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SEQ ID NO: 6	A33	1	W V G K W W P Y L W T C A V R Y T Y D A I S V E T P Q D V L R A S S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L C F I L A I L C S L A L G S V T V H S S E P E V R I P E
SEQ ID NO: 2	45416	1	W G I L G L L G L L G H L T Y D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y O P L
SEQ ID NO: 9	35638	1	W A R R S R H R L L L L R Y L Y V A L G Y H K A Y G F S A P K D O Q V V T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S W I L G S S L Y Q G K G S V Y T A Q S D V Q V P E
A33	51	S R E G L I Q W O K L L L T H E R V V I W P F S H K N Y I H G E L Y K H R V S I S N H A E Q S D A	
40628	43	H N P V K L S C K Y S G F S S P R V E W K F D Q G D T T R L V C Y N H K I T A S Y E D D R V T F L P T	
45416	47	Q G Y T Q V L V K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G O V	
35638	43	Y Q E A I L A C K T P K X T V S S R L E W K K L G R S V S F Y Y Q Q T L Q G D F K N R A E K I D F	
JAM	42	N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D D R V T F S S S	
A33	101	S I T I D Q L T H A D N G T Y E C S V S L . W S D L E G N T K S R Y A L L V L Y P P S K	
40628	93	G I T F K S Y T R E D T G T Y T C H V S E E G G N S Y G E V K Y K L I V L V P P S K	
45416	97	S I Q L S T L E D D O R S H Y T C E V T W O T P D G N Q V V R D K I T E L R V Q K L S V S K P T V T	
35638	93	W I R I K N Y T R S O A G K Y R C E V S A P S E G G N L E E D T Y T L E V L V A P A V	
JAM	92	G I T F S S Y T R K O N G E Y T C H V S E E G G N H Y G E V S I H L T V L Y P P S K	
A33	144	P E C G I E G E T I G N N I O L T C S K E G S P T P O Y S W K R Y N I L N Q E Q	
40628	135	P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M R I S L Q C Q A R . G S P P I S Y I W Y K Q Q T N H Q E P	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F	

FIG. 1A

SEQ ID NO: 6 A33 186 . . . PLA QPAS GQPV S L K N I S T D T S G Y I C T S S N E E G T Q F C H N I T Y
 SEQ ID NO: 1 40628 184 S N S S Y V L H P T T G E L Y F D P L S A S D T G E Y S C E A R N G Y G T P M T S H A V
 SEQ ID NO: 2 45416 188 . . . I K V A T L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D
 SEQ ID NO: 9 35638 186 T N S S Y T M N T K T G T L Q F N T V S K L D T G E Y S C E A R N S V G Y R R C P G K R
 SEQ ID NO: 10 JAM 184 W N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A N G Y G T A M R S E A A

A33 227 A Y R S P S W N Y A L Y G I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A . . .
 40628 228 R H E A V E R N V G Y I V A A Y L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S . . .
 45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T D G Y L G E I S A G P G K S L
 35638 230 . W Q V D D L N I S G I I A A Y V V A V L V I S V C G L G V C Y A K Q R K G Y F S K E T S F Q K S . . .
 JAM 228 H W D A V E L N V G G I V A A V L V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P . .

A33 275 . R P N R E A Y E E P P E Q L R E L S R E E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 40628 275 S K K V I Y S Q P S A R S E E G E F K O T S S F L V
 45416 283 P V F A I I I I S L C C M V V F T H A Y I M L C R K T S Q Q E H V Y E A R
 35638 277 . N S S S K A T T W . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F
 JAM 276 G K K V I Y S Q P S T R A S E E G E F K Q T S S F L V

FIG.-1B

SEQ ID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Vai	Glu	Arg	Lys	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr					
1																	10	15	20	25	30											
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Pro	Arg	Val				
																	35	40	45	50	55	60										
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Arg	Leu	Vai	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Phe	Leu					
																	65	70	75	80	85	90										
Pro	Thr	Gly	Ile	Thr	Rhe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Gly	Gly	Asn	Ser	Tyr	Gly				
																	95	100	105	110	115	120										
Glu	Val	Lys	Val	Lys	Ile	Vai	Val	Leu	Pro	Pro	Ser	Lys	Pro	Thr	Vai	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Arg	Ala	Val				
																	125	130	135	140	145	150										
Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr	Trp	phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr			
																	155	160	165	170	175	180										
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Vai	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr			
																	185	190	195	200	205	210										
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn	Ala	Vai	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val			
																	215	220	225	230	235	240										
Ala	Ala	Vai	Val	Thr	Ile																											
																	245	250	255	260	265	270										
Lys	Gly	Thr	Ser	Ser	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Nrg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	
																	275	280	285	290	295	299										

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FIG._2

SEQ ID NO:2

1 MGIIJLJJJJ CHLTVDTYGR PILEVPESVT GPWKGDVNLP CTYDPLQGYT QVLVVKMLVQR GSDPVТИFLR DSSGDHTIQQA KYQGRLHVSH KVPGDVSSLQL
 101 STLEMDDRSH YTCEVTVWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTGSG YCFTVPQGMR ISLQCQARGG PPISYIWTWQ QTNNQEPIKV ATLSTLLFKP
 ^Glycosaminoglycan attachment site

201 AVIADSGSYF CTAKGQVGSE QHSDIVKFWV KDSKLLKTK TEAPTTMTPY LKATSTVKQS WDWTTDMGY LGETSAGPGK SLPVFAIIIL ISLCCMVWFT
Transmembrane domain

301 MAYIMLCKRT SQQEHVYEEAA R**FIG.-3**OLI2162 (35936.f1)
SEQ ID NO:12

TCGGGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)
SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)
SEQ ID NO:14

ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)
SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

FIG.-8

DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGAG 100
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
 CATCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
 AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGATA 250
 GTGATGCCTA CGAACCCAA AAGCACCCGT GCCTTCAGCA ACTCTCCTA 300
 TGTCCTGAAT CCCACAAACAG GAGAGCTGGT CTTGATCCC CTGTCAGCCT 350
 CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

FIG._4A

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
 TGTGCTCCCT GGCATTGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCCTGT GCCTACTCGG 250
 GCTTTCTTC TCCCCGTGTG GAGTGGAAAGT TTGACCAAGG AGACACCACC 300
 AGACTCGTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
 GACCTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAAGACA 400
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
 GAGGTCAAGG TCAAGCTCAT CGTGTGTG CCTCCATCCA AGCCTACAGT 500
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
 ATAGTGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
 CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700
 CCTCTGATAAC TGGAGAATAC AGCTGT 726

FIG._4B

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
 ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
 TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
 TGACAACCTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
 AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTGGT 300
 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
 TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400
 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
 TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
 GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650
 CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
 AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850
 CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
 CGCCCGCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
 AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000
 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
 CTCTCTTCCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
 GGGAGTCACT GGCTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC 1150
 CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
 TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAAG 1300
 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
 CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400
 TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
 TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
 AAA 1503

FIG._4C

SEQ ID NO:11 GGAGTCCTT CGGGGCTGT TGTGTCAGTG GCCTGATGCC GATGGGACA AAGGCCAAG TCGAGGAA ACTGTTGTGC CTCTTCATAT 100
 TGGGATCCT GTGTCCTC CTGGCATGG CGAGTGTAC AGTGCACCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AACCTGTGA AGTTGTCTG 200
 TGCCTACTCG GGCTTCTCT CTCCCCGTGT GGAGTGGAAAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTTATAATA ACAAGATCAC AGCTTCCTAT 300
 GAGGACGGG TCAACCTCTT GCCAACCTGT AGTCCGTGAC ACGGGAAGAC ACTGGACAT ACACTTGTAT GGTCTCTGAG GAGGGGGCA 400
 ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCCTGT GCCTCATCC AGGCTACAG TAACATCCC CTCTCTGTC ACCATGGGA ACCGGGAGT 500
 GCTGACATGC TCGAAACAAG ATGGTCCCC ACCTTCTGAA TACACTGGT TCAAAAGATGG GATACTGTG CCTACGAATC CCTACGAATC CAAAAGCAC CGGTGCTTC 600
 AGCAACTT CCTATGCTT GAATCCACA ACAGGAGAGC TGGTCTTGA TCCCCTGTCA GCCTCTGATA CGGAGAATA CAGCTGTGAG GCACGGAATG 700
 GGTATGGAC ACCCATGACT TCAAATGCTG TCGGCATGGA AGCTGTTGGAG CGGAATGTCG GGTCATCGT GGCAGCGTC CTGTAACCC TGAATTCTCCT 800
 GGGAAATCTG GTTTGGCA TCTGGTTGCC CTATAGCCGA GGCCACTTTC AGAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT 900
 AGTGCCTGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAT TCCCTGTTGT AGCCTGGTG GCTCACCGCC TATCATCTGC ATTGCTTA CTCAGGTGCT 1000
 ACCGGACTCT GGCCCTGTAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CTTCTACACC CCACAGGGCC CCTACTCTT TCGGATGTGT TTTAATAAT 1100
 GTCAGCTATG TGCCTCATCC TCCCTCATGC CCTCCCTCCC TTCCATACCA CTGCTGAGTG GCCTGAACT TGTTTAAAGT GTTTATTCCTT CATTCTCTTC 1200
 AGGGATCAGG AGGAATCTT GGGTATGCC TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGGGGGT CCCAGGAATC TGCACTCAAC TGCCCACCTG 1300
 GCTGGAGGG ATCTTGAAAT AGGTATCTG AGCTGGTTC TGGGCTCTT CCTTGTGTAC TGACGACCAAG GGCAGGCTGT TCTAGAGGG GAATTAGAGG 1400
 CTAGAGGGC TGAATGGTT GTTGTGAT GACACTGGG TCCCTCCATC TCTGGGGCC ACTCTCTT GTCTCTTCTT GGGAAATGCC ACTGGGATTC 1500
 CTCTGCTG TCCCTCTG TACAAGCTGA CTGACATTGA CTGACATTGA CTGTGTCTGT GAAATATGG AGCTCTTGT GTGGAGAGCA TAGTAAATT TCAGAGAACT 1600
 TGAAGCCAAA AGGATTTAA ACCGGCTGCTC TAAAGAAAG AAAACTGGAG GCTGGGTCAAG CCTGTAATTC CAGAGGCTGA GCGAGGGCA 1700
 TCACTGAGG TCGGGAGTT GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGAAAT ACAAGTTAG CCAGGCTATGG TGGTGCATGC TTGTTGCTCC 1800
 AGCTGCTAG GAGCCCTGGCA ACAAGGAGCA AACTCCAGGT CA 1842

SEQ ID NO:7

1 CCCACCCCTC CGCCCCACGGG TCCCCCACCG CCTCCCCCA CGCTCCCCCA CCACCCAGAG TTTCGCCCTC TTTCGCCCTC TTTCGCCCTC AGAAAGGACA
GGGGGGCCAG GGGGGGGCCAG AGGGGGGTCC GGGGGGGGT GGGGGGGGT AAACCTGGAG AAACCTGGT CTTTCCCTGT TCTTCCCTGT

101 GAACTAGCTC TGGCTGTGAT CCCGATCTTA CTGGCCCTGC TACTCTGGG GCACCTAACCA GTGGACACTT ATGGCCGTC CACCTCGCAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGAGG GTAGGACCTT CACGGTCTCT
1 SEQ ID NO:2 M G I L L G L L P C T Y D P L Q C Y T Q V L V K W L V Q R E S
^MET

201 CTCGAACGG ACCTTGAAA CCCGATCTGA ATCTTCCCTG CACCTATGAC CCCCTCCAAG CCTACACCCA AGCTTGGTG AACCTGGTGG TACAACGTCG
CACATTCCTC TGGAACCTTT CCCCTACACT TAGAACGGAC GTGGGATACTG GGGGACCTTC CGATGTGGCT TCAGAACCCAC TTCAACGGACC ATGGTGGACCC
29 V T C P W K G D V N L P C T Y D P L Q C Y T Q V L V K W L V Q R G

301 CTCAGACCCCT GTCACCATCT TTCTAAGTGA CTCCTCTGGA GACCATATCC AGCAGCCAAA STACCAAGGGC CGCTGTGATG TGAGCCACAA GGTTCCAGGA
GAGCTGGGA CAGTGGTAGA AAGATGCACT GAGAAGACCT CTGCTATAGG TCGCTCCGTTT CATGGTCCC CGGGACTGTAC ACTGGTGTCTT CCAAGGTCTT
62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P C

401 GATGTATCCC TCCAATTGAG CACCTGGAG ATGATGACCC GGAGCCACTA CACGTGTGAA GTCACCTGGC AGACTCTGA TCCCACCCAA GTCGTGAGAG
CTACATACCC ACCGTTAACCTC GTGGGACCTC TACCTACTGG CCTCTGGAT GTGCAACACTT CAGTGGACCC TCTGAGGACT ACCGGTGGTT CAGCACTCTC
95 D V S L Q L S T L E H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGCTC CAAGCCCCACA GTGACAACTG GCACGGGTTA TGGCTTCAAG GTCCCCCAGG GAATGACGAT
TATTCTAATG ACTCGAGGA CAGCTCTTG AGACACAGAG GTTCGGGTGT CACTGTGAC GTGCGCCAAT ACCGAAAGTGC CACGGGTC CCTACTCTA
129 K I T E L R V Q K L S V S K P T V T C S C Y G F T V P Q G H R I

601 TAGCCTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCACT TATATTTGGT ATAACCAACA GACTAATAAC CAGGAACCA TCAAAGTAGG AACCCCTAACT
ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA TATTCTGGGT CTGATTATTC GTCCTTGGGT AGTTTCATCG TTGGGGATTCA
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG._6A

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SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATGCC GACTCGGCT CCTATTCTG CACTGCCAAG CCCACGGCT GCTCTGAGCA CCACAGGAC ATTGTAAGT
TCCAATGAGA AGTTCGGAGC CCACTATCGG CTGACTCCGA CGNTAAAGAC GTGACGGTT CCGGTCNAAC CGAGACTCGT CGTGTGCTG TAACACTTCA
SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTCGCTCAA AGACTCCTCA AGACTACTCA AGACCAAGAC TGACCCACCT ACAACCATAA CATACCCCTT GAAACCAACA TCTACAGTGA AGCAGTCCTG
AACACCAGTT TCTGAGGACT TTGATGAGT TCTGGTCTG ACTTCGGTGA TCTTCTGACT CTATGGAA CTTCGGTGT AGATGTCAGT TCCTCAGGAC
229 V V K D S S K L L K T K T E A P T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTGACATGG ATGGCTACCT TGGAGNACCC AGTGCTGGGC CAGGNNAGG CCTGCCATCA TTGCCCCTGTC TTGCCCCTCATC TCCTCTGCT
CCTGACCTGG TGACTGTACCC TACCGATGGA ACCTCTCTGG TCGAGGACCCG GTCCCTTCTC GGACCCACAG AACCGTAGT AGGAGTAGTA GAGGAACAGC
262 D W T T D M G Y L G E T S A G P K S L P V F A I I L I I S L C

1001 TGTATGGCTG TTTTACCAT GGCCTATATC ATGCTCTGTC CGMAGACATC CCAACNAGAG CATGCTCTAG AGGAGCCAG GTAGAAAGT CTCTCCTCTT
ACATACCAACC AAAATGTTA CGGGATATAG TACGAGATAG CCTTCTCTAG GGTTGTTCTC GTACAGATGC TTGCTGGTC CATTCTTCA GAGGAGGAA
295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGTA CCCCTCCCT CCCCTCAATT TTGATTACTG GGAGGAATG TGGAGAACCC GGGGTGTGGC ACAGACCCCA TCCTAAGCCC GGAGGCTTC
GGTAAAACCT GGGCAGGGA CGGGCAGGGA AACTATGAC CGTCTCTTAC ACCTCCTTC ACCTCCATG TGTCTGGCT AGGATTCCCG CCTCCGGAG
1201 AGGGTCAAGA CATAGCTGCC TTCCCTCTC CAGGCCACCTT CTGAGGTGT TTTGGCCCTC TGACACAM CGATAATTAA GATCCATCTG CCTTCTGCTT
TCCCAGTCT GTATGGACCG AAGGGAGAGA GTCCGTGCAA GACTCCAAACA AAACCGGGAG ACTTGTGTT CCTATTAAAT CTAGGTAGAC CGTTCAGGAA
1301 CCAGAAATCCC TGGGGTAG GATCCCTGATA ATTAAATCGG AAGAATGAG GCAGAAGGT GGGAAACAG GACCAAGCC CCAAGTCCCT TCTTATGGT
GGTCTTGGG ACCCACCATC CTAGGACTAT TAATAACCG TTCTTAACTC CGTCTTCCCA CCCTTGGTC CTGGTGTGG CTGTCAGGAA AGAATACCA

1401 CCTGGGCTCT TGGGCCATAG GGCACATGCC AGAGAGGCC ACCACTCTGG AGAACCTCTG AGGGGGCA TCTTCCAG TGGCTGCTCC ACTGATGAGC
CCACCCGAGA ACCCGTATC CGGTGACCG TCTCTCGGT TCTCTGAGACC TCTTGGTAC TCCCTTCCAC TCCACGGGT AGAAGGGT ACCTACTCTG

1501 CAACTCCCA GAATCTGGEC ACAACTACT CTGATAGCC CTGCTATAGGA CAGGAGTAC AGATCATCGC CGAGATCAAT CGCAACTACG CCCGGCTTGT
CTTGAAGGGT CTTAGACCCG TTGTTGATGAA GACTACTCGG TCTAGTACGG TCTAGTACGG CGTCTAGTA CGTGTGATGC CGGTCAAGGA GGGGGAGGA

FIG.-6B

SEQ ID NO:7

1601 CGACACACTT CCTCTGGATT ATGACTTTCT CCCACACTGAG CCCAAAGTC TCTGTTAAA ATGCCCATTT AGCCAGAT CTCGTACAT AATTGGCCTAG
CCTCTCTCAA CGAGACCTAA TACTAAAGA CCCGTCACTC CGCGTCACTC AGACAAATTG TACCCGGCTAA TCCGGTCTTA GACGACTGTA TTAAACGGATC

1701 TCAGTCCTG CCTCTCTGCAT CCCCTTCTTC CCTGCTACCT CTCTCTCTGG ATAGCCCCAA GTGTCGGCT ACCAACACTG GACCCGCTGG CAGTCACCTGG
ACTCAAGAAC CGAAGACCTA CGGGAAAG CGACGATGCA GACAAGGACC TATCGGGTTT CACAGCCCCA TGCTTGAC CTGGGGACCC CTCAGTGACC

1801 CTTTGCCTG GAATTGCCA GATGGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC GGTTCTTCT GGTAACCTCTC
GAAAGGGAC CTTAAACGGT CTACGTAGAG TTCAATTGGT CGACGACCTA AACCGAGACC CGGAAGACATC ATAGAGACGG CCCCGAAGA CCATGACAG

1901 TCTAAATACC AGACGGAAAGA TCCCCATACC ACTAGGACTT CCTACAGACA CTATTCAACT TTGGCATCTT CCCACCAAGA GACCCGAGG
AGATTATGCC TCTCCCTCTT ACGGGTATCG TGNTCCTGAA CCAGTAGTAC CGATGCTCTGT GATAAGTGA AACCGTAGAA CGGGGTCTT CTGGGCTCCC

2001 AGGGCTCAGCT CTGCCAGCTC AGAGGACCAAG CTATATCCAG CATCATTTCT CTTTCTTCAG GCCCAGACAG CTTTTAATTG AATTGTTAT TTACACGGCC
TCCCCAGTCAA GACGGTCAG TCTCCTGGTC GATATAGCTC CTACTAAGA GAAGGAAGTC CGGGTCTGTC CAAATAAC TTAAACAATA AAATGTCGGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAACT CTAAATCTCT GACTCTCTCTC TGGGCTCTCA TAAATATCTA ATCATACAG C
TCCCCAAGTCA AGACGGAGG CTGATATTCA GATTACAGCA CTGAGAGGG ACCACGAGTT ATTATAGAT TACTATGTC G

FIG.-6C

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCT
 CAGAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGCAGGAGCCACC GCCCTCCTCCT
 GCTGCTGCTGCGTACCTGGTGGTCGCCCTGGCTATCAT AAGGCCTATGGGTTTCTGC
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAA
 AACCCCAAAGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTC
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA
 TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGTGAGTGGGGAAATATCGTTGTGAAGT
 TAGTGCCCCATCTGAGCAAGGCCAAACCTGGAAGAGGGATACTGACTCTGGAAGTATT
 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT
 AGAGCTACGATGTCAAGACAAAGAAGGGAACTCAGCTCCTGAATAACACATGGTTAAGGA
 TGGCATCCGTTGCTAGAAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC
 AATGAATAACAAAATGGAACTCTGCAATTAACTGTTCCAAACTGGACACTGGAGA
 ATATTCCGTGAAGCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
 AGTAGATGATCTAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTAGTGAT
 TTCCGTTGTGGCCTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAAC
 CTCCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTAAAATGTGCAGTG
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGCGGGGGATCACGAGGTCAGGA
 GTTCTAGACCAGTCTGGCCAATATGGTAAACCCCATCTACTAAAATACAAAAATTAG
 CTGGGCATGGTGGCATGTGCCTGCAGTCCAGCTGCTGGAGACAGGAGAATCACTTGA
 ACCCGGGAGGCAGGTTGCAGTGAAGATCACGCCACTGCAGTCCAGCCTGGGTAA
 CAGAGCAAGATTCCATCTAAAAATAAAATAAAATAACTGGTTTAC
 TGTAGAATTCTTACAATAATAGCTTGATATT

FIG._7

SEQ ID NO:9

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
 LEWKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN
 LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
 GIRLLENPR
 LGSQSTNSSYTMNTKTGTLQFNTVSKLDGEYSCEARN
 SVGYRRCPGKRMQVDDLNISGI
 IAAVVVVALVISVCGLGV
 CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPV
 IPALW
 KAAAGGSRGQEF

FIG._11

SEQ ID NO:5

1 CGAGGAAAG TACCAAGGGCC CCCTGCATGT GAGGCCACMAG GTTCAGGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GACCCACTAC
CTGCCGTTTC ATGGTCCCCG CGGACGTACA CTGGCTGTTG CAGGCTCTC TACATAGGG ACGCTCTC TGTTAATCTG TGGGACCTCT ACCTACTGGC CTCGGTGATG
^42257 . f1 SEQ ID NO:18 ^42257 . p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCMACCAAAG TCGTAGAGACA TAAGATTACT GAGCTCGTG TCCAGAACT CTCGTCTCC AACCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CGGTTGCTTC ACCACCTCTCT ATTCCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGGG TTGGGTGTC
^42257 . r1 SEQ ID NO:19

201 TGACAACTGG CAGGGTTAT GGCTTCACGG TGGCCACGG AAATGAGGATT ACCCTTCAT CCCAGGGTTTC CGGTTCTCC TCCCATCAGT TATATTGGT
ACTGTGTGAC CTCGCCAATA CGGAAGTGGC AGGGGTCTCC TTACTCCTAA TCGGAAGTTA CGGTCCAAG CCCCAAGAGG AGGGTAGTC ATATAAACCA

301 ATAAGGAACA GACTAATAAC CAGGGAAACCC ATCAAAAGTAG CHACCCCTAAC TAGCTTACTC TTCAAGCCTG CGGTGATACC CGACTCAGGC TCCTATTCT
TATTGTTGT CTGATTATC GTCCTTGGC TACTTCATC GTGGGATTC ATGGAATCAG AAGTTGGAC GCCACTATCG GCTGAGTCG AGGATAANGA

401 GCACTGCCAA GGGCCAGGTG CGCTCTGAGC AGCACAGCGA CATTGTCAG TTTGTTGCTCA AAGACTCTC AAAGCTACTC AAGACCAAGA CTGAGGGACC
CGTGACCGCTT CCCGGTCCAA CGGAGACTCG TGTTGTCGCT GTCAGCTTC AAAACCAAGT TTTCGATGAG TTCTGTTCT GACTCCGTGC
^42257 . r1 SEQ ID NO:20 ^42257 . f1 SEQ ID NO:20

501 TACAACCATG ACATAACCCCT TGAAGGAAAC ATCTACAGTG AAGGAGCTCT GGACTGGC CACTGACATG GATGGCTTAC CTTGGAGAGAC CAGTCCTGG
ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTCCGTCAGGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACCAACC

601 CAGGAAAGA GCCTGCCCTGT CTTCCTCATCA ATCCCTCATC TCTCTCTGCTG CTGTATGGT GTTTTACCA TGGCTCTAT CATGGCTCTGT CGGAGACAT
GTCCTTCTC CGGACGGACA GAAACGGACA TAGGAGTAAGT AGAGGAACAC GACATACAC CAAAATGGT ACCGGATATA GTACCGAGACA GCCTTCTGTA
^42257 . f2 SEQ ID NO:19

701 CCCAACAAAGA GCATGTCTAC GAAAGGAGCCA GGGCACATGC CAGAGGGCC AAGCAACTCTG GAGAACCAT GAGGCTGGCC ATCTTCGCAA GTGGGTGCTC
GGTTGTTCTC CGTACAGATG CTTCGTCGGT CCCGTGTAAG GTCTCTCCGG TTGCTGAGAC CTCTTGGTA CTCCCACCGG TAGAAGGCTT CACCGACGAG

FIG.- 9A

SEQ ID NO:5

801 CAGTGATGAG CCAAACCTCCC AGAATCTGGG CCAGCAGACTA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCAGATCA ATGGCAACTA
GTCACTACTC GGTTGAAGGG TCTTAGACCC CGTGTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT GGTCTAGT CGGCTCTAGT TACCGTTGAT

901 CGCCCCCTG CTGGACACAG TTCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGTCCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC
GGGGGGGAC GACCTGTGTC AAGGAGACTT AATACTAAA GACCGGTGAC TCCCCTTTC ACAGACAATT TTACGGGT AATCCGGTC TAGACGACTG

1001 ATAATGGCT AGTCAGTCCT TGCCTCTGCC ATGGCCCTTCT TCCCTGCTAC CTCTCTTCTC CGATAGCCA AGTGTCCGC CTACAAACAC TGGAGCCGCT
TATTAACGGA TCACTCAGGA ACGGAAGACG TACCGGAAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGG GATGGTTGTG ACCTCGGGCA

1101 GGGAGTCAT GGTGTTGCC CGGAAATTGTC CAGATGCCATC TCAAGTAAAC CAGCTCTGG ATTGGCTCT CGCCCTCTCT AGTATCTCTG CGGGGGCTT
CCCTCACTGA CGGAAACGGG ACCTTAACAG GTCTACGTAG AGTTCTATTG GTCGCAACG TAAACCGGAC TAAGATAAGA TCATAGACAC GGGCCCGGAA
^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCATA GCACTAGGAC TTGGTCATCA TGCTCTACAGA CACTATTCA CTTGGCCATC TTGCCCACCAAG
GACCATGAGG AGAGATTAT GGTCTCCCTT CTACGGCTAT CGTGATCTG AACCACTAGT ACCGATGTCT GTGATAAGT GAAACCGGTCT AACCTTAACA

1301 AAGACCCGAC GGGAGGCTCA GGTCTGCCAG CTAGAGGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTAA TTGAAATTGT
TTCTGGGCTC CCCTCCCGAGT CGAGACGGTC GAGTCTCTG GTCGATATAG GTCCTAGAA AGAGAAAGAA GTCCGAAATT AACCTTAACA

1401 TATTTCACAG CCAGGGCTTC AGTTCTGCTC CTCACACTATA AGTCTAATGT TCTGACTCTC TCCTGGGTCT CAATAATAT CTAACTAA CAGCAAAAAA
ATAAAGTGTGTC CGGTCCCAAG TCAGAGCGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCAAGA GTTATTATA GATTAGTATT GTCCGTTTTT

1501 AAA
TTT

FIG._ 9B

		FRAME	SCORE	MATCH	PCT
		+1	246	81	30

A33_HUMAN A33 ANTIGEN PRECURSOR - HOMO SAPIENS

A33_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSFGFSSPR---VEM-KFDQGDTTRLV C--YNN

SEQ ID NO:23

A33_human 17 VTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKL LLTHTERVV IWPFSN

SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTFL-----PTGITEFKSVTREDTGTYYTCMV S---EDEGGNSYGEVKVK

A33_human 77 KNYIHIGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVLSMSDLEGNT-KSRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKSTRAFSN

A33_human 135 LLIVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNINLQEQP-----

DNA40628 607 SSYVILNPTTGEV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA

A33_human 187 ---LAQPASGQPVSLKNISTDTSGYI CTSSNEEGTQFCNITVAVRSPSMNVVALYVGIAV

DNA40628 775 AVLVTLLGILVFGIMFAYSRGHFDRT-KKGTSKKVIVSQP

A33_human 244 GVVAALIIIGIIY---CCCCRGKDDNTEDKEDARPNEAYEEP

FIG.- 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19
 IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA40628	112	LCSL--ALGSVTVSSEPEVRIPENNPKLSCAYSGFSSPR---VEW-KFDQGDTTRLV
SEQ ID NO:25		* * * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	12	LCAVRVTVD AISVETPQDVL RASQQKSVTLPCTYHTSTSREGLIQWDKLILLTHTERVV
SEQ ID NO:26		
DNA40628	274	--YNNK--ITAS-YEDRVTFL-----PTGITFKSVTREDTGTYTCTMVSEEGGNSYGEVK
		* * . * * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	72	WPFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECCSVSLMS-DLEGNTK
DNA40628	421	--VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSQDGSPPEYTWFKDGIYMPNPKSTR
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	131	SRVRLIIVLVPPSKPECGLIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNINLQEQP----
DNA40628	595	AFSNSSYVLNPTITGELV-FDPLSASDTGEYSSCEARNGYGTPTMSNAVRMEAVERNVGV--
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	187	LAQPASGQPVSLSKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYV
DNA40628	766	-IVAAVLVTLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIVYSQP
		* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
A33 human	240	GIAVGWVAALLIIIGIITY---CCCCRGRKDDNTEDKEDARPNEAYEEP

FIG._ 10B

SEQID NO: 6 A33_hum 1 M V G K W W P V L W T L C A V R V T V D A I S V E T P O O V L R A S Q G K S Y T L
 SEQID NO: 1 40628 1 W G T K A Q V E R K L L C F I L A I L L C S . . L A L G S V T Y H S S E P E V A R I P E N N P Y K L

A33_hum 42 P C T Y H T S T S S R E G L I O W D K L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I
 40628 49 S C A Y S G F S S P R . . . V E W . K F D O G D T T R L Y C . . Y N N K . . I T A S . Y E D R Y T F

A33_hum 92 S N H A E Q S D A S S I T I D Q L T W A D N G T Y E C S V S L M S D L E G N T K S R V A R L Y L V P P
 40628 90 L P T G I T F K S V I R A E D T G T Y T C H V S E E G G . N S Y G E V K Y K L I Y L V P P

A33_hum 142 S K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N O E Q P
 40628 133 S K P T V N I P S S A T I G N R A V L T C S E O D G S P P S E Y T W F K D G I V W P T N P K S T R A

A33_hum 187 L A Ø P A S G Q P V S L K N I S I D T S G Y Y I C T S S N E E G T Q F C N I T V A V R S
 40628 183 F S N S S Y Y L N P T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P W T S H A V R W E A

A33_hum 231 P S M N V A L Y V G I A V G V V A A L I I G I I Y C C . C C R G K D D N T E D K E D A R P N R E
 40628 232 V E R N V G V . . . I V A A V L V T L I I L G I L V F G I W F I A Y S R A G H F D R T K K G T S S K K V

A33_hum 280 A Y E E P P E Q L R E L S R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 40628 279 I Y S O P S A R S E G E F K O T S S F L V

SEQ ID NO: 6 A33_hum 1 M V G K W W P V L W T L C A Y R V I V D A I S V E I P A D V L R A S Q G K S V T L P C T Y H T S T S
 SEQ ID NO: 2 45416 1 . M G I L L G L L L G H L T V D I Y G R P I L E V P E S V T G P W K G . D V N L P C T Y D P L Q G

A33_hum 51 S R E G L I O W D O K L L L T H T E R V V I W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D
 45416 49 Y T Q V L V K W . L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V . P G D

A33_hum 100 A S I T I D Q L T M A D N G T Y E C S V S . L M S D L E G N T K S A V R U L Y L V P P S
 45416 96 V S L Q L S T L E M D D O R S H Y T C E V T W Q T P D G N Q V V R D K I T E L A V Q K L S V S K P T V

A33_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S
 45416 146 T T G S G Y G F T V P Q G H R I S L o C A A R . G S P P I S Y - W . Y K Q Q T N N Q E P I K V A T

A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T . O F C N I . T V A Y R S P S M N V A L Y V G
 45416 193 L S T L L F K P A V I A D S G S Y F C T A X G Q V G S E O H S D I V K F V V K D S S K L L K T K T E

A33_hum 241 I A V G V V A A I I I G I I I Y C C C C R G K D D O N T E D K E D A R P N R E A Y E E P P E Q L R E
 45416 243 A P T T W T Y P L K A T S T V K Q S W D W T T D W D G Y L G E T S A G P G X S L P V F A I I I S

A33_hum 291 L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q
 45416 293 L C C M V V F T M A Y I M L C A K T S Q Q E H V Y E A R

SEQ ID NO: 6 A33_hum 1 . . . W V G K M W P V [WT] C A V R Y T V O . . . A I S V E T P Q D V L R A S O G K S V T L P C
SEQ ID NO: 9 35638 1 M A R R S H A R L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y Q E A I L A C

A33_hum 44 T Y H T S T S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N
35638 51 . . . K T P K K T V S S R L E W K K L . . . G R S V V S F V Y Y Q Q T . L Q G D . F K N R

A33_hum 94 N A E Q S D A S I T I D O L T M A D N G T Y E C S S L M S D O L E G N . T K S A V R L Y L V P P S
35638 87 . A E N I D F N I R I K N V T R S D A G K Y R C E V S A P S E Q G A N L E E D O T V T L E V L V A P A

A33_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P O Y S W K R Y N I L N O E Q P L A Q P A S
35638 136 V P S C E V P S S A L S G T V V E L L R C Q D G E N P A P E Y T W F K D G I R L L E N P R L G S O S

A33_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V . . . R S P S M N V A L Y V
35638 186 T N S S Y T M N T K T G I L Q F N T . V S K L D T G E Y S C E A R N S V G Y R A C P G K R M Q V D D

A33_hum 240 G I A V G Y V A L I I G I I I Y C C . . . C C A R G K D D N T E D K E D A R P N R E A Y E E P P E
35638 235 L N I S G I I A V V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33_hum 287 Q L R E L S R . E R E E E D D Y R Q E E Q R S T G R E S P D H L D O
35638 285 W S E N V Q O W L T P V I P A L W K A A A G G S R G O E F

19 / 24

SEQ ID NO: 10 jam
SEQ ID NO: 1 40628

W G T E C K A G R K L L F L F T . S H I L C S L V Y O G K G S V T A Q S D V Q Y P E N E S I K L F C
W G T K A Q V E R K L L C L F I L A I L C S L A I G S V T V H S S E P E V R I P E N N P V K L S C

jam
40628

1
1

D N G E Y T C M V S E E G G O N Y G E V S I H T V L V P P S K P T I S V P S S V T I G N R A V
O T G T Y T C M V S E E G G O N S Y G E V K V K T V N I P S S A T I G N R A V

jam 1
40628 1

T C S E H D G S P P S E Y S W F K D G I .	S M L T A D A K X T R A F M N S S S F T I D P K S G D L - F
T C S E O D G S P P S E Y T W F K D G I .	V M P T N P K S T R A F S N S S Y V L N P T T G E L V F

jam 2
40628 2

P Y T A F D S G E Y C O A N G Y G T A M R S E A H M O A V E L N V G G I V A A V L V T L L P L S A D T G E Y S C E A R N G Y G T P M T S N A V R M E A V E R N V G V I V A V I V T L L

jam 2
40628 2

G	L	I	F	G	V	W	F	A	Y	S	R	G	Y	F	E	T	T	K	K	G	T	A	P	G	K	K	V	I	Y	S	O	P	S	T	R	E	G	E	F	K	O	T	S	S	F	L	
G	L	I	V	F	G	I	W	F	A	Y	S	R	G	H	F	D	R	T	K	K	G	T	.	S	S	K	K	V	I	Y	S	O	P	S	A	R	E	G	E	F	K	O	T	S	S	F	L

jam 3 40628

FIG. - 15

FIG.-15

jam	49	C T Y S . . . C F S S P R Y E W X F V O G S T T A L Y . . . C Y N S Q I . - T A P Y A D R V T F S .
45416	41	C T Y D P L O G Y T Q V L Y K W L V O R G S D P V T I F L R D S S G O H I Q Q A K Y Q G R L H V S H

jam	90 S S G I T F S S Y T A K D N G E Y T C W V . . . S E E G G O N Y G E V S I H L T Y L
45416	91	K V P G O V S L O L S T L E M D O R A S H Y T C E V T W Q T P G N Q V R O D K I T T E L A Y Q K L S V

jam	132	SKPT	ISVPS	...	SYTIGNRAYLTCS	SEHDTCSEHDTCS	GSPPS	SEYSWF	KDGISMLTADA
45446	141	SKPT	VTTG	SCYGFTY	PQGMRI	SYIWYK	SYI	QOQTNNOEOP	CAR.

jam	178	K K T R A F M N S S F T I D P K S G D L I F D P V T A F D S G E Y C O A O N G Y G T A M R S E A A
45416	188	I K V A T L S T L L F X P A D S G S Y F C T A K G O V G S E O H S D I V

jam	228	H . . . N D A V E L N V G G I V A A V L V T I L G L L I F G . . . V W F A Y S A G Y F E T T K K
	45416	227 K F V V V K D S S K U L K T K T E A P T T M T Y P L X A T S T V K O S S W D M T T D N D G Y L G E T S A

jam 272 G T A P G K K V I Y S S O P S T R S E G E F K Q T S S F L Y
45416 277 G P G K S L P V F A I L I S L C C M V V F T W A Y I M L C R A K T S Q Q E H V Y E A R

SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F L F T S W H I L G S L V Q G K G S V Y T A Q S D V A V . . . P E N E S I K L
SEQ ID NO: 29	35638	1	W A R R S R H A R L L L L R Y L V V A L G Y H K A Y G F S A P X D Q Q V U T A V E Y Q E A I L
jam	48	T C . T Y S G F S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G J T F S	
35638	49	A C K T P K K T V S S R L E W K K L . G R A S V S F Y Y Q Q T L Q G D F K N R A E M I D F N I R I K	
jam	97	S V T R K D N G E Y T C W V S . . E E G G A N Y G E V S I H L T V L V P P S K P T I S V P S S V T I	
35638	98	N V T A S D A G K Y R A C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S	
jam	145	G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S	
35638	148	G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L . E N P R I G S Q S T N S Y T M N T K T	
jam	195	G O L I F D P Y T A F D S G E Y Y C O A O N G Y G I T A M R S E A A H M D A V E L N V G G I V A A V L	
35638	197	G T L O F N T V S K L D T G E Y S C E A R N S V G . Y A R C P G K R M O V D D L N I S G I I A A V V	
jam	245	V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T R S E G E F K Q	
35638	246	V V A L V I S V C G G l G Y C Y A Q R K G Y F . . . S K E T S F Q K S N S S S K A T T M S E N V Q O W L	
jam	295	T S S F L V	
35638	293	T P V I P A L W K A A A G G S A G Q E F	

FIG.- 17

SEQ ID NO: 6 A33_hum 1 W V G K W P V L W T . L C A V R V T V D A I S V E T P O D V L R A S Q G K S V T L P C T
SEQ ID NO: 10 jam 1 W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q S D V Q V P E N E S I K L R C T

A33_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N A V S I S N N
jam 51 Y S G F S S P R Y E W . K F V Q G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33_hum 95 A E Q S D A S I T I D Q L T W A D O N G T Y E C S V S L M S D O L E G N T K S R V R A L L V L V P P S K P
jam 91 S G I T F S S V T R K D O N G E Y T C H V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33_hum 145 E C G I E G E T I I G N N I O L T C O S K E G S P T P Q Y S W K R Y N I L N O E Q P L A Q P A S G Q
jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F H

A33_hum 195 P V S L K N I S T D T S G Y Y I C T S N E E G T O F C N I T V A V R S P S M N V A L
jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A Y E L

A33_hum 238 Y V . G I A V G V V A A L I I G I I Y C C C C C A G K D D N T E D A R P N R E A Y E E
jam 235 N Y G G I I V A A V L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K K V I Y S Q

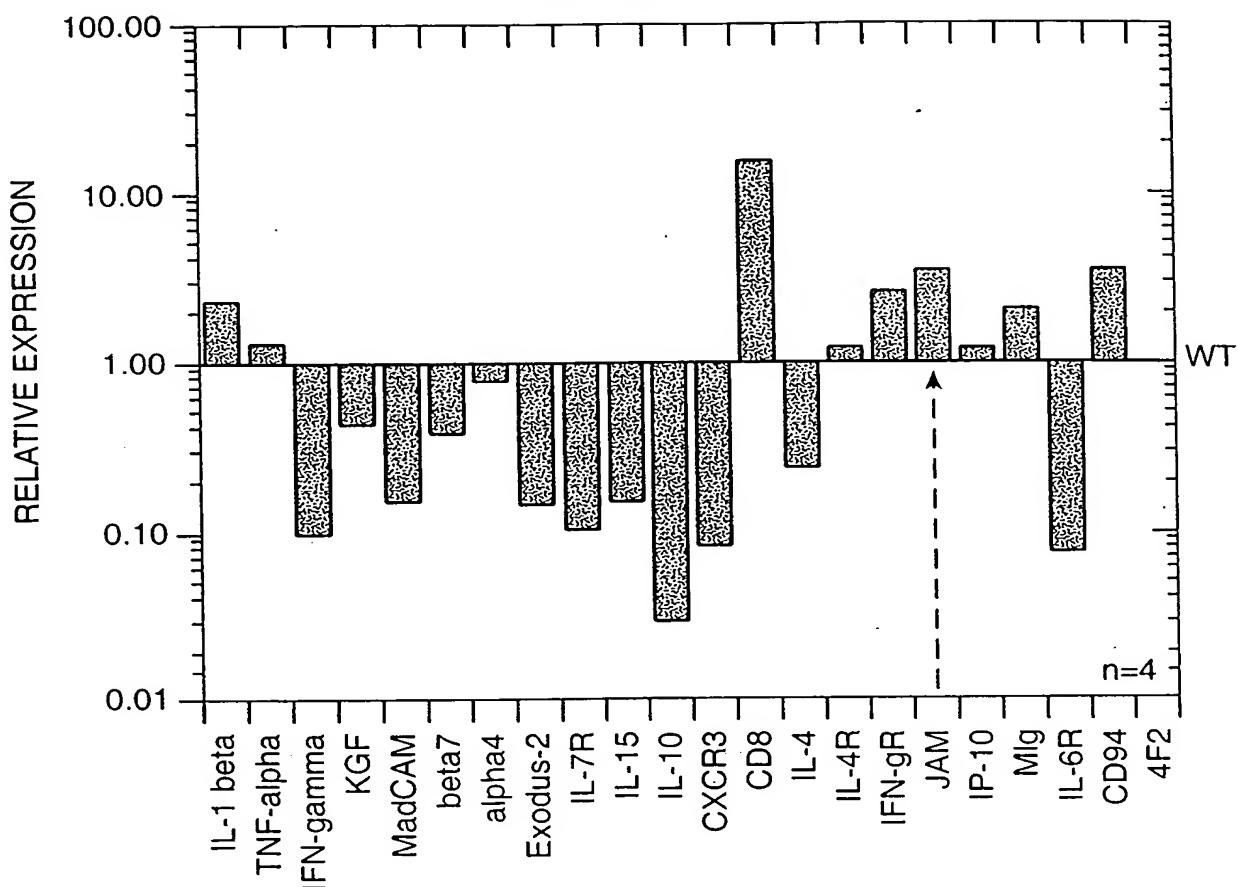
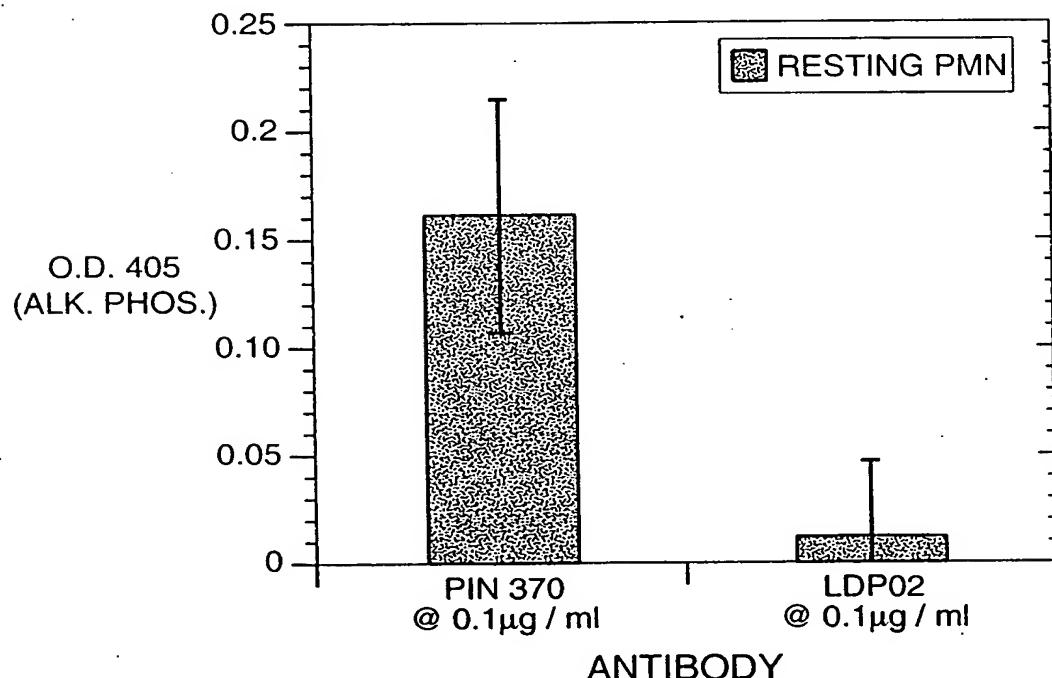
A33_hum 284 P P E O L R E L S R E R E E E D O Y R Q E E Q R S T G R E S P D H L D O
jam 284 P S T A S E G E F K Q T S S F L V

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++	APPENDIX	+
PUTAMEN	+	OVARY	++	LUNG	++++
SUSTANTIA NIGRA	+	PANCREAS	++	TRACHEA	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	PLACENTA	++++
THalamus	+	ADRENAL GLAND	++		
NUCLEUS ACCUMBENS	+	THYROID GLAND	++	FETAL BRAIN	+
SPINAL CORD	-	SALIVARY GLAND	++	FETAL HEART	+
		MAMMARY GLAND	++	FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

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FIG.- 19

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**FIG._20****FIG._21**